

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/319,831BDATE: 08/16/96
TIME: 11:03:22

INPUT SET: S12193.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

A/6

SEQUENCE LISTING

(1) General Information:

ENTERED

- (i) APPLICANT: Hewick, Rodney M.
Wang, Jack H.
Wozney, John M.
Celeste, Anthony J.

(ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/319,831
(B) FILING DATE: 6-OCT-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI 5182A-DIV

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-876-1170
(B) TELEFAX: 617-876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/319,831BDATE: 08/16/96
TIME: 11:03:25

INPUT SET: S12193.raw

47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: unknown
49
50 (ii) MOLECULE TYPE: peptide
51
52 (iii) HYPOTHETICAL: NO
53
54 (iv) ANTI-SENSE: NO
55
56 (vi) ORIGINAL SOURCE:
57 (F) TISSUE TYPE: Bone
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
62 1 5 10 15
63
64 Val Ile Ala Pro Gln Gly Tyr
65 20
66
67 (2) INFORMATION FOR SEQ ID NO:2:
68
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 18 amino acids
71 (B) TYPE: amino acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: unknown
74
75 (ii) MOLECULE TYPE: peptide
76
77 (iii) HYPOTHETICAL: NO
78
79 (iv) ANTI-SENSE: NO
80
81 (v) FRAGMENT TYPE: internal
82
83 (vi) ORIGINAL SOURCE:
84 (A) ORGANISM: Bos taurus
85 (F) TISSUE TYPE: Bone
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
89
90 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
91 1 5 10 15
92
93 Leu Arg
94
95
96 (2) INFORMATION FOR SEQ ID NO:3:
97
98 (i) SEQUENCE CHARACTERISTICS:
99 (A) LENGTH: 7 amino acids

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/319,831BDATE: 08/16/96
TIME: 11:03:29

INPUT SET: S12193.raw

100 (B) TYPE: amino acid
101 (C) STRANDEDNESS: single
102 (D) TOPOLOGY: unknown
103
104 (ii) MOLECULE TYPE: peptide
105
106 (iii) HYPOTHETICAL: NO
107
108 (iv) ANTI-SENSE: NO
109
110 (vi) ORIGINAL SOURCE:
111 (A) ORGANISM: Bos taurus
112 (F) TISSUE TYPE: Bone
113
114
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
116
117 Ala Cys Cys Ala Pro Thr Lys
118 1 5
119
120 (2) INFORMATION FOR SEQ ID NO:4:
121
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 23 amino acids
124 (B) TYPE: amino acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: unknown
127
128 (ii) MOLECULE TYPE: peptide
129
130 (iii) HYPOTHETICAL: NO
131
132 (vi) ORIGINAL SOURCE:
133 (A) ORGANISM: Bos taurus
134 (F) TISSUE TYPE: Bone
135
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
138
139 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
140 1 5 10 15
141
142 Val His Gly Ser His Gly Arg
143 20
144
145 (2) INFORMATION FOR SEQ ID NO:5:
146
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 80 base pairs
149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: double
151 (D) TOPOLOGY: linear
152

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/319,831BDATE: 08/16/96
TIME: 11:03:32

INPUT SET: S12193.raw

153 (ii) MOLECULE TYPE: DNA (genomic)
154
155 (iii) HYPOTHETICAL: NO
156
157 (iv) ANTI-SENSE: NO
158
159 (vi) ORIGINAL SOURCE:
160 (A) ORGANISM: Bos taurus
161
162 (vii) IMMEDIATE SOURCE:
163 (B) CLONE: acc30
164
165 (viii) POSITION IN GENOME:
166 (C) UNITS: bp
167
168 (ix) FEATURE:
169 (A) NAME/KEY: CDS
170 (B) LOCATION: 25..57
171
172
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
176 Lys Leu Ser Ala Thr Ser Val Leu Tyr
177 1 5
178
179 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80
180 Tyr Asp
181 10
182
183
184 (2) INFORMATION FOR SEQ ID NO:6:
185
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 11 amino acids
188 (B) TYPE: amino acid
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: protein
192
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
194
195 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
196 1 5 10
197
198 (2) INFORMATION FOR SEQ ID NO:7:
199
200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 199 base pairs
202 (B) TYPE: nucleic acid
203 (C) STRANDEDNESS: double
204 (D) TOPOLOGY: linear
205

RAW SEQUENCE LISTING PATENT APPLICATION US/08/319,831B

 DATE: 08/16/96
 TIME: 11:03:36

INPUT SET: S12193.raw

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206      (ii) MOLECULE TYPE: DNA (genomic)
207
208      (iii) HYPOTHETICAL: NO
209
210      (vi) ORIGINAL SOURCE:
211          (A) ORGANISM: Bos taurus
212
213      (vii) IMMEDIATE SOURCE:
214          (A) LIBRARY: Bovine genomic
215          (B) CLONE: Lambda 9800-10
216
217      (viii) POSITION IN GENOME:
218          (C) UNITS: bp
219
220      (ix) FEATURE:
221          (A) NAME/KEY: exon
222          (B) LOCATION: 30..199
223
224      (ix) FEATURE:
225          (A) NAME/KEY: intron
226          (B) LOCATION: 1..29
227
228      (ix) FEATURE:
229          (A) NAME/KEY: CDS
230          (B) LOCATION: 30..179
231
232
233      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
234
235      TGCCCGCTGC CCCCTCCCGC CCCC GCCAG GTG CAC CTG CTG AAG CCG CAC GCG      53
236                                     Val His Leu Leu Lys Pro His Ala
237                                     1                      5
238
239      GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG      101
240      Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
241          10                      15                      20
242
243      CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC      149
244      Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
245          25                      30                      35                      40
246
247      ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCCA ACTCCACCGG      196
248      Met Val Val Arg Ala Cys Gly Cys His
249          45                      50
250
251      CAG      199
252
253
254      (2) INFORMATION FOR SEQ ID NO:8:
255
256          (i) SEQUENCE CHARACTERISTICS:
257              (A) LENGTH: 49 amino acids
258              (B) TYPE: amino acid
  
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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/319,831B

DATE: 08/16/96
TIME: 11:03:39

INPUT SET: S12193.raw

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Original Text